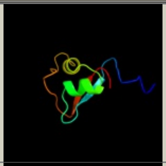
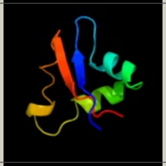
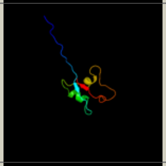
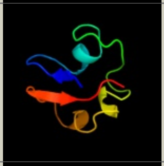
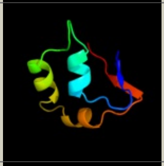
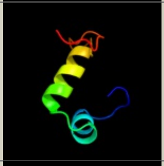
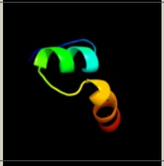
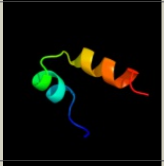
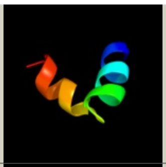
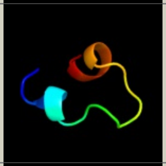
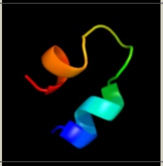
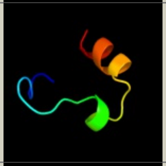
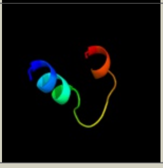
Email	l.a.kelley@imperial.ac.uk
Description	P0ADE6
Date	Wed Jan 25 15:20:27 GMT 2012
Unique Job ID	7fcfdbe54943d64f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l9yA_	Alignment		99.6	32	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cvnh-lysm lectin; **PDBTitle:** solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)
2	d1e0ga_	Alignment		99.5	27	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
3	c2djpA_	Alignment		99.5	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sb145; **PDBTitle:** the solution structure of the lysm domain of human2 hypothetical protein sb145
4	d1y7ma2	Alignment		99.4	34	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
5	c2gu1A_	Alignment		98.7	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
6	c1y7mB_	Alignment		98.1	33	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14040; **PDBTitle:** crystal structure of the b. subtilis ykud protein at 2 a2 resolution
7	c2elhA_	Alignment		34.9	4	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
8	d1k78a1	Alignment		26.3	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
9	d1y0pa3	Alignment		26.2	14	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
10	c2r0qF_	Alignment		21.4	26	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
11	c2lfcA_	Alignment		17.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase, flavoprotein subunit; **PDBTitle:** solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j

12	d2ofya1	Alignment		16.2	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
13	d1siga_	Alignment		15.2	11	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
14	c2a6eF_	Alignment		14.6	16	**PDB header:**transferase **Chain:** F: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** crystal structure of the t. thermophilus rna polymerase2 holoenzyme
15	d1smyf3	Alignment		13.5	16	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
16	d1ku2a2	Alignment		13.3	15	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
17	d1iyjb3	Alignment		13.0	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
18	d1hlva1	Alignment		12.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
19	d2cx1a1	Alignment		12.3	30	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
20	d1bxla_	Alignment		11.3	4	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
21	d1rr7a_	Alignment	not modelled	11.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
22	c1rr7A_	Alignment	not modelled	11.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
23	c1ku2A_	Alignment	not modelled	11.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sigma factor siga; **PDBTitle:** crystal structure of thermus aquaticus rna polymerase sigma2 subunit fragment containing regions 1.2 to 3.1
24	d1d4ca3	Alignment	not modelled	10.6	32	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
25	c2yv6A_	Alignment	not modelled	10.4	4	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**bcl-2 homologous antagonist/killer; **PDBTitle:** crystal structure of human bcl-2 family protein bak
26	c1l9uH_	Alignment	not modelled	10.3	16	**PDB header:**transcription **Chain:** H: **PDB Molecule:**sigma factor siga; **PDBTitle:** thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
27	d6paxa1	Alignment	not modelled	10.2	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
28	c2w48D_	Alignment	not modelled	10.1	15	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2

						regulator sorc from klebsiella pneumoniae
29	d1miua3	Alignment	not modelled	9.7	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
30	d1bw6a_	Alignment	not modelled	9.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
31	c3d79A_	Alignment	not modelled	9.3	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph0734; **PDBTitle:** crystal structure of hypothetical protein ph0734.1 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
32	d1g5ma_	Alignment	not modelled	8.9	4	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
33	d1o0la_	Alignment	not modelled	8.7	4	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
34	c2o2fA_	Alignment	not modelled	8.5	4	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand
35	c2gm4B_	Alignment	not modelled	8.2	24	**PDB header:**recombination, dna **Chain:** B: **PDB Molecule:**transposon gamma-delta resolvase; **PDBTitle:** an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
36	d1zy3a1	Alignment	not modelled	8.2	4	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
37	d2bt6a1	Alignment	not modelled	8.0	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
38	c2x48B_	Alignment	not modelled	7.8	21	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
39	d2ponb1	Alignment	not modelled	7.6	4	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
40	d2fug33	Alignment	not modelled	7.4	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
41	c3f56F_	Alignment	not modelled	7.0	32	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**csos1d; **PDBTitle:** the structure of a previously undetected carboxysome shell2 protein: csos1d from prochlorococcus marinus med4
42	c2xa0A_	Alignment	not modelled	7.0	4	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** crystal structure of bcl-2 in complex with a bax bh32 peptide
43	c2vofA_	Alignment	not modelled	7.0	4	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**bcl-2-related protein a1; **PDBTitle:** structure of mouse a1 bound to the puma bh3-domain
44	d1u9ka_	Alignment	not modelled	6.6	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
45	c3t76A_	Alignment	not modelled	6.6	26	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
46	c1y6uA_	Alignment	not modelled	6.5	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excisionase from transposon tn916; **PDBTitle:** the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
47	d1ysga1	Alignment	not modelled	6.1	4	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
48	c3b7hA_	Alignment	not modelled	5.9	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
49	c1zs7A_	Alignment	not modelled	5.9	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ape0525; **PDBTitle:** the structure of gene product ape0525 from aeropyrum pernix
50	c2rrdA_	Alignment	not modelled	5.9	7	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hrdc domain from bloom syndrome protein; **PDBTitle:** structure of hrdc domain from human bloom syndrome protein, blm
51	c2kpjA_	Alignment	not modelled	5.8	6	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa; **PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
52	d1pq1a_	Alignment	not modelled	5.7	4	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
53	c2rn7A_	Alignment	not modelled	5.4	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**is629 orfa; **PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
54	c2aukA_	Alignment	not modelled	5.4	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain;

						PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
55	d1jala2	Alignment	not modelled	5.4	36	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
56	d1y9qa2	Alignment	not modelled	5.3	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
57	d1wi0a_	Alignment	not modelled	5.3	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
58	d1p9ka_	Alignment	not modelled	5.3	18	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
59	c3clcC_	Alignment	not modelled	5.2	25	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
60	c2yxyA_	Alignment	not modelled	5.2	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein, gk0453; **PDBTitle:** crystarl structure of hypothetical conserved protein, gk0453
61	c1u78A_	Alignment	not modelled	5.1	8	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
62	c2ewtA_	Alignment	not modelled	5.1	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd